

PAGE: 1

**RAW SEQUENCE LISTING  
PATENT APPLICATION US/08/591,447A**DATE: 12/10/97  
TIME: 15:13:45**INPUT SET: S22013.raw**

This Raw Listing contains the General  
Information Section and up to the first 54 pages.

1                   **SEQUENCE LISTING**  
2  
3     (1)    **General Information:**  
4  
5         (i)   **APPLICANT:** QUENTIN-MILLET al., Marie-Jose et  
6  
7         (ii)   **TITLE OF INVENTION:** TBP2 FRAGMENTS OF THE TRANSFERRIN  
8                    RECEPTOR OF NEISSERIA MENINGITIDIS  
9  
10      (iii)   **NUMBER OF SEQUENCES:** 44  
11  
12      (iv)   **CORRESPONDENCE ADDRESS:**  
13         (A)   **ADDRESSEE:** LARSON AND TAYLOR  
14         (B)   **STREET:** 1199 NORTH FAIRFAX STREET  
15         (C)   **CITY:** ALEXANDRIA  
16         (D)   **STATE:** VIRGINIA  
17         (E)   **COUNTRY:** USA  
18         (F)   **ZIP:** 22314  
19  
20      (v)   **COMPUTER READABLE FORM:**  
21         (A)   **MEDIUM TYPE:** Floppy disk  
22         (B)   **COMPUTER:** IBM PC compatible  
23         (C)   **OPERATING SYSTEM:** PC-DOS/MS-DOS  
24         (D)   **SOFTWARE:** PatentIn Release #1.0, Version #1.30  
25  
26      (vi)   **CURRENT APPLICATION DATA:**  
27         (A)   **APPLICATION NUMBER:** US 08/591,447  
28         (B)   **FILING DATE:** 29-JAN-1996  
29         (C)   **CLASSIFICATION:**  
30  
31      (viii)   **ATTORNEY/AGENT INFORMATION:**  
32         (A)   **NAME:** SARRO, THOMAS P  
33         (B)   **REGISTRATION NUMBER:** 19,196  
34         (C)   **REFERENCE/DOCKET NUMBER:** XI/P02956  
35  
36      (ix)   **TELECOMMUNICATION INFORMATION:**  
37         (A)   **TELEPHONE:** 703-739-4900  
38         (B)   **TELEFAX:** 703-739-9577  
39  
40  
41      (2)   **INFORMATION FOR SEQ ID NO:1:**  
42  
43         (i)   **SEQUENCE CHARACTERISTICS:**  
44         (A)   **LENGTH:** 2230 base pairs  
45         (B)   **TYPE:** nucleic acid  
46         (C)   **STRANDEDNESS:** single

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**RAW SEQUENCE LISTING  
PATENT APPLICATION US/08/591,447A**DATE: 12/10/97  
TIME: 15:13:48**INPUT SET: S22013.raw**

47                   (D) TOPOLOGY: linear  
48  
49                   (ii) MOLECULE TYPE: DNA (genomic)  
50  
51                   (vi) ORIGINAL SOURCE:  
52                    (A) ORGANISM: Neisseria meningitidis  
53                    (B) STRAIN: IM2169  
54  
55                   (ix) FEATURE:  
56                    (A) NAME/KEY: sig\_peptide  
57                    (B) LOCATION: 60..119  
58  
59                   (ix) FEATURE:  
60                    (A) NAME/KEY: mat\_peptide  
61                    (B) LOCATION: 120..2192  
62  
63                   (ix) FEATURE:  
64                    (A) NAME/KEY: CDS  
65                    (B) LOCATION: 60..2192  
66  
67                   (ix) FEATURE:  
68                    (A) NAME/KEY: misc\_feature  
69                    (B) LOCATION: 120..1154  
70  
71                   (ix) FEATURE:  
72                    (A) NAME/KEY: misc\_feature  
73                    (B) LOCATION: 1155..1748  
74  
75                   (ix) FEATURE:  
76                    (A) NAME/KEY: misc\_feature  
77                    (B) LOCATION: 1749..2192  
78  
79                   (ix) FEATURE:  
80                    (A) NAME/KEY: misc\_binding  
81                    (B) LOCATION: 237..1169  
82  
83  
84                   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:  
85  
86 ATTTGTTAAA AATAAAATAAA ATAATAATCC TTATCATTCT TTAATTGAAT TGGGTTTAT       59  
87  
88 ATG AAC AAT CCA TTG GTA AAT CAG GCT GCT ATG GTG CTG CCT GTG TTT       107  
89 Met Asn Asn Pro Leu Val Asn Gln Ala Ala Met Val Leu Pro Val Phe  
90 -20               -15               -10               -5  
91  
92 TTG TTG AGT GCC TGT CTG GGC GGC GGC AGT TTC GAT CTT GAT TCT       155  
93 Leu Leu Ser Ala Cys Leu Gly Gly Gly Ser Phe Asp Leu Asp Ser  
94               1               5               10  
95  
96 GTC GAT ACC GAA GCC CCG CGT CCC GCG CCA AAG TAT CAA GAT GTT TCT       203  
97 Val Asp Thr Glu Ala Pro Arg Pro Ala Pro Lys Tyr Gln Asp Val Ser  
98               15               20               25  
99

**RAW SEQUENCE LISTING  
PATENT APPLICATION US/08/591,447A**

DATE: 12/10/97  
TIME: 15:13:50

**INPUT SET: S22013.raw**

100	TCC GAA AAA CCG CAA GCC CAA AAA GAC CAA GGC GGA TAC GGT TTT GCG	251
101	Ser Glu Lys Pro Gln Ala Gln Lys Asp Gln Gly Gly Tyr Gly Phe Ala	
102	30 35 40	
103		
104	ATG AGG TTG AAA CGG AGG AAT TGG TAT CCG GGG GCA GAA GAA AGC GAG	299
105	Met Arg Leu Lys Arg Arg Asn Trp Tyr Pro Gly Ala Glu Glu Ser Glu	
106	45 50 55 60	
107		
108	GTT AAA CTG AAC GAG AGT GAT TGG GAG GCG ACG GGA TTG CCG ACA AAA	347
109	Val Lys Leu Asn Glu Ser Asp Trp Glu Ala Thr Gly Leu Pro Thr Lys	
110	65 70 75	
111		
112	CCC AAG GAA CTT CCT AAA CGG CAA AAA TCG GTT ATT GAA AAA GTA GAA	395
113	Pro Lys Glu Leu Pro Lys Arg Gln Lys Ser Val Ile Glu Lys Val Glu	
114	80 85 90	
115		
116	ACA GAC GGC GAC AGC GAT ATT TAT TCT TCC CCC TAT CTC ACA CCA TCA	443
117	Thr Asp Gly Asp Ser Asp Ile Tyr Ser Ser Pro Tyr Leu Thr Pro Ser	
118	95 100 105	
119		
120	AAC CAT CAA AAC GGC AGC GCT GGC AAC GGT GTA AAT CAA CCT AAA AAT	491
121	Asn His Gln Asn Gly Ser Ala Gly Asn Gly Val Asn Gln Pro Lys Asn	
122	110 115 120	
123		
124	CAG GCA ACA GGT CAC GAA AAT TTC CAA TAT GTT TAT TCC GGT TGG TTT	539
125	Gln Ala Thr Gly His Glu Asn Phe Gln Tyr Val Tyr Ser Gly Trp Phe	
126	125 130 135 140	
127		
128	TAT AAA CAT GCA GCG AGT GAA AAA GAT TTC AGT AAC AAA AAA ATT AAG	587
129	Tyr Lys His Ala Ala Ser Glu Lys Asp Phe Ser Asn Lys Lys Ile Lys	
130	145 150 155	
131		
132	TCA GGC GAC GAT GGT TAT ATC TTC TAT CAC GGT GAA AAA CCT TCC CGA	635
133	Ser Gly Asp Asp Gly Tyr Ile Phe Tyr His Gly Glu Lys Pro Ser Arg	
134	160 165 170	
135		
136	CAA CTT CCT GCT TCT GGA AAA GTT ATC TAC AAA GGT GTG TGG CAT TTT	683
137	Gln Leu Pro Ala Ser Gly Lys Val Ile Tyr Lys Gly Val Trp His Phe	
138	175 180 185	
139		
140	GTA ACC GAT ACA AAA AAG GGT CAA GAT TTT CGT GAA ATT ATC CAG CCT	731
141	Val Thr Asp Thr Lys Lys Gly Gln Asp Phe Arg Glu Ile Ile Gln Pro	
142	190 195 200	
143		
144	TCA AAA AAA CAA GGC GAC AGG TAT AGC GGA TTT TCT GGT GAT GGC AGC	779
145	Ser Lys Lys Gln Gly Asp Arg Tyr Ser Gly Phe Ser Gly Asp Gly Ser	
146	205 210 215 220	
147		
148	GAA GAA TAT TCC AAC AAA AAC GAA TCC ACG CTG AAA GAT GAT CAC GAG	827
149	Glu Glu Tyr Ser Asn Lys Asn Glu Ser Thr Leu Lys Asp Asp His Glu	
150	225 230 235	
151		
152	GGT TAT GGT TTT ACC TCG AAT TTA GAA GTG GAT TTC GGC AAT AAG AAA	875

**RAW SEQUENCE LISTING  
PATENT APPLICATION US/08/591,447A**

DATE: 12/10/97  
TIME: 15:13:52

**INPUT SET: S22013.raw**

153	Gly Tyr Gly Phe Thr Ser Asn Leu Glu Val Asp Phe Gly Asn Lys Lys			
154	240	245	250	
155				
156	TTG ACG GGT AAA TTA ATA CGC AAT AAT GCG AGC CTA AAT AAT AAT ACT		923	
157	Leu Thr Gly Lys Leu Ile Arg Asn Asn Ala Ser Leu Asn Asn Asn Thr			
158	255	260	265	
159				
160	AAT AAT GAC AAA CAT ACC ACC CAA TAC TAC AGC CTT GAT GCA CAA ATA		971	
161	Asn Asn Asp Lys His Thr Thr Gln Tyr Tyr Ser Leu Asp Ala Gln Ile			
162	270	275	280	
163				
164	ACA GGC AAC CGC TTC AAC GGC ACG GCA ACG GCA ACT GAC AAA AAA GAG		1019	
165	Thr Gly Asn Arg Phe Asn Gly Thr Ala Thr Ala Thr Asp Lys Lys Glu			
166	285	290	295	300
167				
168	AAT GAA ACC AAA CTA CAT CCC TTT GTT TCC GAC TCG TCT TCT TTG AGC		1067	
169	Asn Glu Thr Lys Leu His Pro Phe Val Ser Asp Ser Ser Ser Leu Ser			
170	305	310	315	
171				
172	GGC GGC TTT TTC GGC CCG CAG GGT GAG GAA TTG GGT TTC CGC TTT TTG		1115	
173	Gly Gly Phe Phe Gly Pro Gln Gly Glu Glu Leu Gly Phe Arg Phe Leu			
174	320	325	330	
175				
176	AGC GAC GAT CAA AAA GTT GCC GTT GTC GGC AGC GCG AAA ACC AAA GAC		1163	
177	Ser Asp Asp Gln Lys Val Ala Val Val Gly Ser Ala Lys Thr Lys Asp			
178	335	340	345	
179				
180	AAA CTG GAA AAT GGC GCG GCG GCT TCA GGC AGC ACA GGT GCG GCA GCA		1211	
181	Lys Leu Glu Asn Gly Ala Ala Ser Gly Ser Thr Gly Ala Ala Ala			
182	350	355	360	
183				
184	TCG GGC GGT GCG GCA GGC ACG TCG TCT GAA AAC AGT AAG CTG ACC ACG		1259	
185	Ser Gly Gly Ala Ala Gly Thr Ser Ser Glu Asn Ser Lys Leu Thr Thr			
186	365	370	375	380
187				
188	GTT TTG GAT GCG GTT GAA TTG ACA CTA AAC GAC AAG AAA ATC AAA AAT		1307	
189	Val Leu Asp Ala Val Glu Leu Thr Leu Asn Asp Lys Lys Ile Lys Asn			
190	385	390	395	
191				
192	CTC GAC AAC TTC AGC AAT GCC GCC CAA CTG GTT GTC GAC GGC ATT ATG		1355	
193	Leu Asp Asn Phe Ser Asn Ala Ala Gln Leu Val Val Asp Gly Ile Met			
194	400	405	410	
195				
196	ATT CCG CTC CTG CCC AAG GAT TCC GAA AGC GGG AAC ACT CAG GCA GAT		1403	
197	Ile Pro Leu Leu Pro Lys Asp Ser Glu Ser Gly Asn Thr Gln Ala Asp			
198	415	420	425	
199				
200	AAA GGT AAA AAC GGC GGA ACA GAA TTT ACC CGC AAA TTT GAA CAC ACG		1451	
201	Lys Gly Lys Asn Gly Gly Thr Glu Phe Thr Arg Lys Phe Glu His Thr			
202	430	435	440	
203				
204	CCG GAA AGT GAT AAA AAA GAC GCC CAA GCA GGT ACG CAG ACG AAT GGG		1499	
205	Pro Glu Ser Asp Lys Asp Ala Gln Ala Gly Thr Gln Thr Asn Gly			

**RAW SEQUENCE LISTING  
PATENT APPLICATION US/08/591,447A**

 DATE: 12/10/97  
 TIME: 15:13:54
**INPUT SET: S22013.raw**

206	445	450	455	460	
207					
208	GCG CAA ACC GCT TCA AAT ACG GCA GGT GAT ACC AAT GGC AAA ACA AAA				1547
209	Ala Gln Thr Ala Ser Asn Thr Ala Gly Asp Thr Asn Gly Lys Thr Lys				
210	465	470	475		
211					
212	ACC TAT GAA GTC GAA GTC TGC TGT TCC AAC CTC AAT TAT CTG AAA TAC				1595
213	Thr Tyr Glu Val Glu Val Cys Cys Ser Asn Leu Asn Tyr Leu Lys Tyr				
214	480	485	490		
215					
216	GGA ATG TTG ACG CGC AAA AAC AGC AAG TCC GCG ATG CAG GCA GGA GGA				1643
217	Gly Met Leu Thr Arg Lys Asn Ser Lys Ser Ala Met Gln Ala Gly Gly				
218	495	500	505		
219					
220	AAC AGT AGT CAA GCT GAT GCT AAA ACG GAA CAA GTT GAA CAA AGT ATG				1691
221	Asn Ser Ser Gln Ala Asp Ala Lys Thr Glu Gln Val Glu Gln Ser Met				
222	510	515	520		
223					
224	TTC CTC CAA GGC GAG CGT ACC GAT GAA AAA GAG ATT CCA ACC GAC CAA				1739
225	Phe Leu Gln Gly Glu Arg Thr Asp Glu Lys Glu Ile Pro Thr Asp Gln				
226	525	530	535	540	
227					
228	AAC GTC GTT TAT CGG GGG TCT TGG TAC GGG CAT ATT GCC AAC GGC ACA				1787
229	Asn Val Val Tyr Arg Gly Ser Trp Tyr Gly His Ile Ala Asn Gly Thr				
230	545	550	555		
231					
232	AGC TGG AGC GGC AAT GCT TCT GAT AAA GAG GGC GGC AAC AGG GCG GAA				1835
233	Ser Trp Ser Gly Asn Ala Ser Asp Lys Glu Gly Gly Asn Arg Ala Glu				
234	560	565	570		
235					
236	TTT ACT GTG AAT TTT GCC GAT AAA AAA ATT ACC GGC AAG TTA ACC GCT				1883
237	Phe Thr Val Asn Phe Ala Asp Lys Lys Ile Thr Gly Lys Leu Thr Ala				
238	575	580	585		
239					
240	GAA AAC AGG CAG GCG CAA ACC TTT ACC ATT GAG GGA ATG ATT CAG GGC				1931
241	Glu Asn Arg Gln Ala Gln Thr Phe Thr Ile Glu Gly Met Ile Gln Gly				
242	590	595	600		
243					
244	AAC GGC TTT GAA GGT ACG GCG AAA ACT GCT GAG TCA GGT TTT GAT CTC				1979
245	Asn Gly Phe Glu Gly Thr Ala Lys Thr Ala Glu Ser Gly Phe Asp Leu				
246	605	610	615	620	
247					
248	GAT CAA AAA AAT ACC ACC CGC ACG CCT AAG GCA TAT ATC ACA GAT GCC				2027
249	Asp Gln Lys Asn Thr Thr Arg Thr Pro Lys Ala Tyr Ile Thr Asp Ala				
250	625	630	635		
251					
252	AAG GTA AAG GGC GGT TTT TAC GGG CCT AAA GCC GAA GAG TTG GGC GGA				2075
253	Lys Val Lys Gly Gly Phe Tyr Gly Pro Lys Ala Glu Glu Leu Gly Gly				
254	640	645	650		
255					
256	TGG TTT GCC TAT CCG GGC GAT AAA CAA ACG GAA AAG GCA ACA GCT ACA				2123
257	Trp Phe Ala Tyr Pro Gly Asp Lys Gln Thr Glu Lys Ala Thr Ala Thr				
258	655	660	665		

PAGE: 1

**SEQUENCE VERIFICATION REPORT  
PATENT APPLICATION US/08/591,447A**

DATE: 12/10/97  
TIME: 15:13:57

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